

I. AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-42 (cancelled)

43. (new) A method of removing contaminating nucleic acids from a sample and then analyzing the sample comprising the steps of chemically treating the sample, wherein the chemical treatment results in the chemical modification of the contaminating nucleic acid and then analyzing the sample.

44. (new) The method according to claim 43, wherein the chemical modification renders the contaminating nucleic acids removable from the sample.

45. (new) The method according to claim 43, wherein the chemical treatment comprises the use of sodium hydroxide, sodium hypochlorite, sodium metabisulphite or ammonium metabisulphite.

46. (new) The method according to claim 43, further comprising the step of treating the sample with uracil glycosylase.

47. (new) A method according to claim 43, wherein the contaminating nucleic acid is selected from the group consisting of: deoxyribonucleic acid (DNA), ribonucleic acid (RNA), locked nucleic acid (LNA) and protein nucleic acid (PNA).

48. (new) The method according to claim 43, wherein the contaminating nucleic acid is an amplicon derived from a PCR, another DNA amplification process or is artificially created.

49. (new) The method according to claim 43, wherein the contaminating nucleic acid is synthetic.
50. (new) A method of analyzing a nucleic acid sample for genomic DNA comprising the steps of
- (i) chemically treating the sample, wherein the chemical treatment results in the chemical modification of contaminating nucleic acid;
 - (ii) treating the sample with an enzyme; and
 - (iii) characterizing the treated sample for the genomic DNA.
51. (new) The method according to claim 50, wherein the enzyme is uracil glycolase.
52. (new) The method according to claim 50, wherein the genomic DNA in the treated nucleic acid sample is characterized by a method selected from the group of: PCR, mitochondrial DNA sequencing, single nucleotide polymorphism (SNP) analysis and low copy number PCR.
53. (new) The method of claim 43, wherein the sample is obtained from a crime scene or other sites away from the crime scene with forensic value relevant to the crime.
54. (new) The method according to claim 43, wherein the sample is selected from the grouping consisting of: blood, saliva, hair, semen, urine, faeces, bone, agricultural and veterinary samples.
55. (new) The method according to claim 43, wherein the detection is carried out for forensic use.
56. (new) The method of claim 50, wherein the sample is obtained from a crime scene or other sites away from the crime scene with forensic value relevant to the crime.

57. (new) The method according to claim 50, wherein the sample is selected from the grouping consisting of: blood, saliva, hair, semen, urine, faeces, bone, agricultural and veterinary samples.
58. (new) The method according to claim 50, wherein the detection is carried out for forensic use.
59. (new) A method of removing contaminating nucleic acids from a sample and then analyzing the sample comprising the step of enzymatically treating the sample, wherein the enzymatic treatment results in the inactivation of the contaminating nucleic acid.
60. (new) The method according to claim 59, wherein the enzymatic treatment requires the use of methylation specific restriction enzymes.
61. (new) A method of removing contaminating nucleic acids from a sample and then analyzing the sample comprising the steps of physically treating the sample, wherein the physical treatment results in the removal of the contaminating nucleic acid, and then analyzing the sample.
62. (new) The method according to claim 61, wherein the physical treatment is the physical binding of nucleic acids bases to a methylation specific region.
63. The method according to claim 62, wherein the nucleic acid bases are a probe specific for the methylation specific region.
64. (new) A database comprising the results generated from the method according to claim 43.